

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:	Kapeller-Libermann, Rosana, et al.		
Application No.:	09/935,290	Group No.:	1652
Filed:	August 21, 2001	Examiner:	Nashed, N. T.
For:	56919, A NOVEL HUMAN ACYLTRANSFERASE AND USES THEREOF		

Mail Stop AF  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

SUBMISSION OF "SEQUENCE LISTING," COMPUTER READABLE COPY,  
AND/OR AMENDMENT PERTAINING THERETO  
FOR BIOTECHNOLOGY INVENTION CONTAINING NUCLEOTIDE  
AND/OR AMINO ACID SEQUENCE

1. ☐ This submission accompanies the new application being filed concurrently herewith.  
☒ This replies to the Telephone discussion with Examiner Nashed September 20, 2005.

## IDENTIFICATION OF PERSON MAKING STATEMENT

2. I, Kerri Pollard Schray  
(type or print name of person signing below)

state the following:

## ITEMS BEING SUBMITTED

## CERTIFICATION UNDER 37 C.F.R. SECTIONS 1.8(a) and 1.10\*

I hereby certify that, on the date shown below, this correspondence is being:

## DELIVERY

- ☒ delivered BY HAND to the United States Patent and Trademark Office in an envelope addressed to Mail Stop AF, Commissioner for Patents.  
37 C.F.R. SECTION 1.8(a)

## 37 C.F.R. SECTION 1.10\*

- ☐ with sufficient postage as first class mail. ☐ as "Express Mail Post Office to Addressee" Mailing Label No.

## TRANSMISSION

- ☐ transmitted by facsimile to the Patent and Trademark Office.

Signature

*For C. Itendley*  
For C. Itendley

Date: September 23, 2005

(type or print name of person certifying)

**\*WARNING:** Each paper or fee filed by "Express Mail" must have the number of the "Express Mail" mailing label placed thereon prior to mailing. 37 C.F.R. section 1.10(b). "Since the filing of correspondence under section 1.10 without the Express Mail mailing label thereon is an oversight that can be avoided by the exercise of reasonable care, requests for waiver of this requirement will not be granted on petition." Notice of Oct. 24, 1996, 60 Fed. Reg. 56,439, at 56,442.

**ITEMS BEING SUBMITTED**

3. Submitted herewith is/are:

- A. ☒ "Sequence Listing(s)" for the nucleotide and/or amino acid sequence(s) in this application. Each sequence in the "Sequence Listing" is assigned a separate identifier as required in 37 C.F.R. Section 1.821(c) and 37 C.F.R. Sections 1.822 and 1.823.
- B. ☐ An amendment to the description and/or claims, wherein reference is made to the sequence by use of the assigned identifier, as required in 37 C.F.R. Section 1.821(d).
- C. ☐ A copy of each "Sequence Listing" submitted for this application in computer readable form, in accordance with the requirements of 37 C.F.R. Sections 1.821(e) and 1.824.
- D. ☐ Please transfer to this application, in accordance with 37 C.F.R. Section 1.821(e), the computer readable copy(ies) from applicant's other application identified as follows:

In re application of:			
Application No.:		Group No.:	
Filed:		Examiner:	
For:			

The Computer readable form(s) of applicant's other application corresponds to the "Sequence Identifier(s)" of the application as follows:

Computer Readable Form	"Sequence Identifier"
(other application)	(this application)

- E. ☒ A statement that the content of each "Sequence Listing" submitted and each computer readable copy are the same, as required in 37 C.F.R. Section 1.821(g).
- ☐ Because the statement is not made by a person registered to practice before the Office, the Statement is verified as required in 37 C.F.R. Section 1.821(b).
- F. ☒ Because this submission is made in fulfilling the requirement under 37 C.F.R. Section 1.821(g), a statement that the submission includes no new matter.
- ☐ Because the statement is not made by a person registered to practice before the Office, the statement is verified, as required in 37 C.F.R. Section 1.821(g).

**STATEMENT THAT "SEQUENCE LISTING"  
AND COMPUTER READABLE COPY ARE THE SAME  
AND/OR THAT PAPERS SUBMITTED INCLUDES NO NEW MATTER**

4. I hereby state:

- A. ☒ Each computer readable form submitted in this application, including those forms requested to be transferred from applicant's other application, is the same as the "Sequence Listing" to which it is indicated to relate.
- B. ☒ All papers accompanying this submission, or for which a request for transfer from applicants' other application, introduce no new matter.

**EXTENSION OF TERM**

5. The proceedings herein are for a patent application and the provisions of 37 C.F.R. Section 1.136 apply.

- (a) ☐ Applicant petitions for an extension of time under 37 C.F.R. Section 1.136 (fees: 37 C.F.R. Section 1.17(a)(1)-(4)) for the total number of months checked below:

<u>Extension (months)</u>	<u>Fee for other than small entity</u>	<u>Fee for small entity</u>
<input type="checkbox"/> one month	\$ 120.00	\$ 60.00
<input type="checkbox"/> two months	\$ 450.00	\$ 225.00
<input type="checkbox"/> three months	\$1,020.00	\$ 510.00
<input type="checkbox"/> four months	\$1,590.00	\$ 795.00

Fee \$0.00

If an additional extension of time is required, please consider this a petition therefor.

- ☐ An extension for \_\_\_\_\_ months has already been secured, and the fee paid therefor of \$0.00 is deducted from the total fee due for the total months of extension now requested.

Extension fee due with this request \$0.00

**OR**

- (b) ☒ Applicant believes that no extension of term is required. However, this conditional petition is being made to provide for the possibility that applicant has inadvertently overlooked the need for a petition and fee for extension of time.

Practitioner's Docket No. MPI00-343P1RRCEM

**FEE PAYMENT**

6. ☐ Attached is a check in the sum of \$ \_\_\_\_\_ .
- ☐ Charge Account No. 501668 the sum of \$0.00 .  
A duplicate of this transmittal is attached.

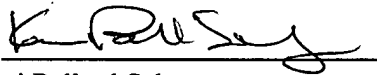
**FEE DEFICIENCY**

8. ☒ If any additional extension and/or fee is required, charge Account No. 501668 .
9. Correspondence Address  
Direct all future correspondence to:

Customer Number 30405  
OR  
Intellectual Property Department  
MILLENNIUM PHARMACEUTICALS, INC.  
40 Landsdowne Street  
Cambridge, MA 02139

September 23, 2005

MILLENNIUM PHARMACEUTICALS, INC.

By   
Kerri Pollard Schray  
Registration No. 47,066  
40 Landsdowne Street  
Cambridge, MA 02139  
Telephone – (617) 551-3676  
Facsimile – (617) 551-8820

# SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana

<120> 56919, A NOVEL HUMAN ACYLTRANSFERASE AND  
USES THEREOF

<130> MPI00-343P1RM

<140> 09/935,290

<141> 2001-08-21

<150> 60/226,509

<151> 2000-08-21

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3003

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (341)...(2827)

<221> misc\_feature

<222> 2939, 2973

<223> n = A,T,C or G

<400> 1

```

ttcggcacca ggctgctgcg gggggactct ttctgaggtt actgtggagc acccaaagtc 60
tgtcagcctc tggccgtgca aacaggcacc cagaggaacc agaccttgct tattcaccca 120
cagcctggga ctgtcttctc cagagtctcc atcagctttg ctaatcgact gattggaaat 180
aattcctcaa acaccaccaa gtcaaggata caggcagcag cggctcccct gttgtatgga 240
cattctgcac ccgaaactga tagctgagtc ctgaagtttt atgttatgaa acagaagaac 300
tttcatccca gcacatgatt tgggaattac actttgtgac atg gat gaa tct gca 355
                                     Met Asp Glu Ser Ala
                                     1 5

```

```

ctg acc ctt ggt aca ata gat gtt tct tat ctg cca cat tca tca gaa 403
Leu Thr Leu Gly Thr Ile Asp Val Ser Tyr Leu Pro His Ser Ser Glu
                10                15                20

```

```

tac agt gtt ggt cga tgt aag cac aca agt gag gaa tgg ggt gag tgt 451
Tyr Ser Val Gly Arg Cys Lys His Thr Ser Glu Glu Trp Gly Glu Cys
                25                30                35

```

```

ggc ttt aga ccc acc gtc ttc aga tct gca act tta aaa tgg aaa gaa 499
Gly Phe Arg Pro Thr Val Phe Arg Ser Ala Thr Leu Lys Trp Lys Glu
                40                45                50

```

```

agc cta atg agt cgg aaa agg cca ttt gtt gga aga tgt tgt tac tcc 547
Ser Leu Met Ser Arg Lys Arg Pro Phe Val Gly Arg Cys Cys Tyr Ser
                55                60                65

```

```

tgc act ccc cag agc tgg gac aaa ttt ttc aac ccc agt atc ccg tct 595
Cys Thr Pro Gln Ser Trp Asp Lys Phe Phe Asn Pro Ser Ile Pro Ser
                70                75                80                85

```

ttg ggt ttg cgg aat gtt att tat atc aat gaa act cac aca aga cac	643
Leu Gly Leu Arg Asn Val Ile Tyr Ile Asn Glu Thr His Thr Arg His	
90 95 100	
cgc gga tgg ctt gca aga cgc ctt tct tac gtt ctt ttt att caa gag	691
Arg Gly Trp Leu Ala Arg Arg Leu Ser Tyr Val Leu Phe Ile Gln Glu	
105 110 115	
cga gat gtg cat aag ggc atg ttt gcc acc aat gtg act gaa aat gtg	739
Arg Asp Val His Lys Gly Met Phe Ala Thr Asn Val Thr Glu Asn Val	
120 125 130	
ctg aac agc agt aga gta caa gag gca att gca gaa gtg gct gct gaa	787
Leu Asn Ser Ser Arg Val Gln Glu Ala Ile Ala Glu Val Ala Ala Glu	
135 140 145	
tta aac cct gat ggt tct gcc cag cag caa tca aaa gcc gtt aac aaa	835
Leu Asn Pro Asp Gly Ser Ala Gln Gln Gln Ser Lys Ala Val Asn Lys	
150 155 160 165	
gtg aaa aag aaa gct aaa agg att ctt caa gaa atg gtt gcc act gtc	883
Val Lys Lys Lys Ala Lys Arg Ile Leu Gln Glu Met Val Ala Thr Val	
170 175 180	
tca ccg gca atg atc aga ctg act ggg tgg gtg ctg cta aaa ctg ttc	931
Ser Pro Ala Met Ile Arg Leu Thr Gly Trp Val Leu Leu Lys Leu Phe	
185 190 195	
aac agc ttc ttt tgg aac att caa att cac aaa ggt caa ctt gag atg	979
Asn Ser Phe Phe Trp Asn Ile Gln Ile His Lys Gly Gln Leu Glu Met	
200 205 210	
gtt aaa gct gca act gag acg aat ttg ccg ctt ctg ttt cta cca gtt	1027
Val Lys Ala Ala Thr Glu Thr Asn Leu Pro Leu Leu Phe Leu Pro Val	
215 220 225	
cat aga tcc cat att gac tat ctg ctg ctc act ttc att ctc ttc tgc	1075
His Arg Ser His Ile Asp Tyr Leu Leu Leu Thr Phe Ile Leu Phe Cys	
230 235 240 245	
cat aac atc aaa gca cca tac att gct tca ggc aat aat ctc aac atc	1123
His Asn Ile Lys Ala Pro Tyr Ile Ala Ser Gly Asn Asn Leu Asn Ile	
250 255 260	
cca atc ttc agt acc ttg atc cat aag ctt ggg ggc ttc ttc ata cga	1171
Pro Ile Phe Ser Thr Leu Ile His Lys Leu Gly Gly Phe Phe Ile Arg	
265 270 275	
cga agg ctc gat gaa aca cca gat gga cgg aaa gat gtt ctc tat aga	1219
Arg Arg Leu Asp Glu Thr Pro Asp Gly Arg Lys Asp Val Leu Tyr Arg	
280 285 290	
gct ttg ctc cat ggg cat ata gtt gaa tta ctt cga cag cag caa ttc	1267
Ala Leu Leu His Gly His Ile Val Glu Leu Leu Arg Gln Gln Gln Phe	
295 300 305	
ttg gag atc ttc ctg gaa ggc aca cgt tct agg agt gga aaa acc tct	1315
Leu Glu Ile Phe Leu Glu Gly Thr Arg Ser Arg Ser Gly Lys Thr Ser	
310 315 320 325	
tgt gct cgg gca gga ctt ttg tca gtt gtg gta gat act ctg tct acc	1363
Cys Ala Arg Ala Gly Leu Leu Ser Val Val Val Asp Thr Leu Ser Thr	
330 335 340	

aat gtc atc cca gac atc ttg ata ata cct gtt gga atc tcc tat gat	1411
Asn Val Ile Pro Asp Ile Leu Ile Ile Pro Val Gly Ile Ser Tyr Asp	
345 350 355	
cgc att atc gaa ggt cac tac aat ggt gaa caa ctg ggc aaa cct aag	1459
Arg Ile Ile Glu Gly His Tyr Asn Gly Glu Gln Leu Gly Lys Pro Lys	
360 365 370	
aag aat gag agc ctg tgg agt gta gca aga ggt gtt att aga atg tta	1507
Lys Asn Glu Ser Leu Trp Ser Val Ala Arg Gly Val Ile Arg Met Leu	
375 380 385	
cga aaa aac tat ggt tgt gtc cga gtg gat ttt gca cag cca ttt tcc	1555
Arg Lys Asn Tyr Gly Cys Val Arg Val Asp Phe Ala Gln Pro Phe Ser	
390 395 400 405	
tta aag gaa tat tta gaa agc caa agt cag aaa ccg gtg tct gct cta	1603
Leu Lys Glu Tyr Leu Glu Ser Gln Ser Gln Lys Pro Val Ser Ala Leu	
410 415 420	
ctt tcc ctg gag caa gcg ttg tta cca gct ata ctt cct tca aga ccc	1651
Leu Ser Leu Glu Gln Ala Leu Leu Pro Ala Ile Leu Pro Ser Arg Pro	
425 430 435	
agt gat gct gct gat gaa ggt aga gac acg tcc att aat gag tcc aga	1699
Ser Asp Ala Ala Asp Glu Gly Arg Asp Thr Ser Ile Asn Glu Ser Arg	
440 445 450	
aat gca aca gat gaa tcc cta cga agg agg ttg att gca aat ctg gct	1747
Asn Ala Thr Asp Glu Ser Leu Arg Arg Arg Leu Ile Ala Asn Leu Ala	
455 460 465	
gag cat att cta ttc act gct agc aag tcc tgt gcc att atg tcc aca	1795
Glu His Ile Leu Phe Thr Ala Ser Lys Ser Cys Ala Ile Met Ser Thr	
470 475 480 485	
cac att gtg gct tgc ctg ctc ctc tac aga cac agg cag gga att gat	1843
His Ile Val Ala Cys Leu Leu Leu Tyr Arg His Arg Gln Gly Ile Asp	
490 495 500	
ctc tcc aca ttg gtc gaa gac ttc ttt gtg atg aaa gag gaa gtc ctg	1891
Leu Ser Thr Leu Val Glu Asp Phe Phe Val Met Lys Glu Glu Val Leu	
505 510 515	
gct cgt gat ttt gac ctg ggg ttc tca gga aat tca gaa gat gta gta	1939
Ala Arg Asp Phe Asp Leu Gly Phe Ser Gly Asn Ser Glu Asp Val Val	
520 525 530	
atg cat gcc ata cag ctg ctg gga aat tgt gtc aca atc acc cac act	1987
Met His Ala Ile Gln Leu Leu Gly Asn Cys Val Thr Ile Thr His Thr	
535 540 545	
agc agg aac gat gag ttt ttt atc acc ccc agc aca act gtc cca tca	2035
Ser Arg Asn Asp Glu Phe Phe Ile Thr Pro Ser Thr Thr Val Pro Ser	
550 555 560 565	
gtc ttc gaa ctc aac ttc tac agc aat ggg gta ctt cat gtc ttt atc	2083
Val Phe Glu Leu Asn Phe Tyr Ser Asn Gly Val Leu His Val Phe Ile	
570 575 580	
atg gag gcc atc ata gct tgc agc ctt tat gca gtt ctg aac aag agg	2131
Met Glu Ala Ile Ile Ala Cys Ser Leu Tyr Ala Val Leu Asn Lys Arg	
585 590 595	

gga ctg ggg ggt ccc act agc acc cca cct aac ctg atc agc cag gag	2179
Gly Leu Gly Gly Pro Thr Ser Thr Pro Pro Asn Leu Ile Ser Gln Glu	
600 605 610	
cag ctg gtg cgg aag gcg gcc agc ctg tgc tac ctt ctc tcc aat gaa	2227
Gln Leu Val Arg Lys Ala Ala Ser Leu Cys Tyr Leu Leu Ser Asn Glu	
615 620 625	
ggc acc atc tca ctg cct tgc cag aca ttt tac caa gtc tgc cat gaa	2275
Gly Thr Ile Ser Leu Pro Cys Gln Thr Phe Tyr Gln Val Cys His Glu	
630 635 640 645	
aca gta gga aag ttt atc cag tat ggc att ctt aca gtg gca gag cac	2323
Thr Val Gly Lys Phe Ile Gln Tyr Gly Ile Leu Thr Val Ala Glu His	
650 655 660	
gat gac cag gaa gat atc agt cct agt ctt gct gag cag cag tgg gac	2371
Asp Asp Gln Glu Asp Ile Ser Pro Ser Leu Ala Glu Gln Gln Trp Asp	
665 670 675	
aag aag ctt cca gaa cct ttg tct tgg aga agt gat gaa gaa gat gaa	2419
Lys Lys Leu Pro Glu Pro Leu Ser Trp Arg Ser Asp Glu Glu Asp Glu	
680 685 690	
gac agt gac ttt ggg gag gaa cag cga gat tgc tac ctg aag gtg agc	2467
Asp Ser Asp Phe Gly Glu Glu Gln Arg Asp Cys Tyr Leu Lys Val Ser	
695 700 705	
caa tcc aag gag cac cag cag ttt atc acc ttc tta cag aga ctc ctt	2515
Gln Ser Lys Glu His Gln Gln Phe Ile Thr Phe Leu Gln Arg Leu Leu	
710 715 720 725	
ggg cct ttg ctg gag gcc tac agc tct gct gcc atc ttt gtt cac aac	2563
Gly Pro Leu Leu Glu Ala Tyr Ser Ser Ala Ala Ile Phe Val His Asn	
730 735 740	
ttc agt ggt cct gtt cca gaa cct gag tat ctg caa aag ttg cac aaa	2611
Phe Ser Gly Pro Val Pro Glu Pro Glu Tyr Leu Gln Lys Leu His Lys	
745 750 755	
tac cta ata acc aga aca gaa aga aat gtt gca gta tat gct gag agt	2659
Tyr Leu Ile Thr Arg Thr Glu Arg Asn Val Ala Val Tyr Ala Glu Ser	
760 765 770	
gcc aca tat tgt ctt gtg aag aat gct gtg aaa atg ttt aag gat att	2707
Ala Thr Tyr Cys Leu Val Lys Asn Ala Val Lys Met Phe Lys Asp Ile	
775 780 785	
ggg gtt ttc aag gag acc aaa caa aag aga gtg tct gtt tta gaa ctg	2755
Gly Val Phe Lys Glu Thr Lys Gln Lys Arg Val Ser Val Leu Glu Leu	
790 795 800 805	
agc agc act ttt cta cct caa tgc aac cga caa aaa ctt cta gaa tat	2803
Ser Ser Thr Phe Leu Pro Gln Cys Asn Arg Gln Lys Leu Leu Glu Tyr	
810 815 820	
att ctg agt ttt gtg gtg ctg tag gtaacgtgtg gcactgctgg caaatgaagg	2857
Ile Leu Ser Phe Val Val Leu *	
825	
tcatgagatg agttccttgt aggtaccagc ttctggctca agagtttgaa ggtgccttcg	2917
caggggtcag gcctgccttg tncogaagtg atctcctgga agacaagtgc cttctncctc	2977
catggatctg agatcttccc agcttt	3003



<210> 2  
 <211> 828  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Met Asp Glu Ser Ala Leu Thr Leu Gly Thr Ile Asp Val Ser Tyr Leu  
 1 5 10 15  
 Pro His Ser Ser Glu Tyr Ser Val Gly Arg Cys Lys His Thr Ser Glu  
 20 25 30  
 Glu Trp Gly Glu Cys Gly Phe Arg Pro Thr Val Phe Arg Ser Ala Thr  
 35 40 45  
 Leu Lys Trp Lys Glu Ser Leu Met Ser Arg Lys Arg Pro Phe Val Gly  
 50 55 60  
 Arg Cys Cys Tyr Ser Cys Thr Pro Gln Ser Trp Asp Lys Phe Phe Asn  
 65 70 75 80  
 Pro Ser Ile Pro Ser Leu Gly Leu Arg Asn Val Ile Tyr Ile Asn Glu  
 85 90 95  
 Thr His Thr Arg His Arg Gly Trp Leu Ala Arg Arg Leu Ser Tyr Val  
 100 105 110  
 Leu Phe Ile Gln Glu Arg Asp Val His Lys Gly Met Phe Ala Thr Asn  
 115 120 125  
 Val Thr Glu Asn Val Leu Asn Ser Ser Arg Val Gln Glu Ala Ile Ala  
 130 135 140  
 Glu Val Ala Ala Glu Leu Asn Pro Asp Gly Ser Ala Gln Gln Gln Ser  
 145 150 155 160  
 Lys Ala Val Asn Lys Val Lys Lys Lys Ala Lys Arg Ile Leu Gln Glu  
 165 170 175  
 Met Val Ala Thr Val Ser Pro Ala Met Ile Arg Leu Thr Gly Trp Val  
 180 185 190  
 Leu Leu Lys Leu Phe Asn Ser Phe Phe Trp Asn Ile Gln Ile His Lys  
 195 200 205  
 Gly Gln Leu Glu Met Val Lys Ala Ala Thr Glu Thr Asn Leu Pro Leu  
 210 215 220  
 Leu Phe Leu Pro Val His Arg Ser His Ile Asp Tyr Leu Leu Leu Thr  
 225 230 235 240  
 Phe Ile Leu Phe Cys His Asn Ile Lys Ala Pro Tyr Ile Ala Ser Gly  
 245 250 255  
 Asn Asn Leu Asn Ile Pro Ile Phe Ser Thr Leu Ile His Lys Leu Gly  
 260 265 270  
 Gly Phe Phe Ile Arg Arg Arg Leu Asp Glu Thr Pro Asp Gly Arg Lys  
 275 280 285  
 Asp Val Leu Tyr Arg Ala Leu Leu His Gly His Ile Val Glu Leu Leu  
 290 295 300  
 Arg Gln Gln Gln Phe Leu Glu Ile Phe Leu Glu Gly Thr Arg Ser Arg  
 305 310 315 320  
 Ser Gly Lys Thr Ser Cys Ala Arg Ala Gly Leu Leu Ser Val Val Val  
 325 330 335  
 Asp Thr Leu Ser Thr Asn Val Ile Pro Asp Ile Leu Ile Ile Pro Val  
 340 345 350  
 Gly Ile Ser Tyr Asp Arg Ile Ile Glu Gly His Tyr Asn Gly Glu Gln  
 355 360 365  
 Leu Gly Lys Pro Lys Lys Asn Glu Ser Leu Trp Ser Val Ala Arg Gly  
 370 375 380  
 Val Ile Arg Met Leu Arg Lys Asn Tyr Gly Cys Val Arg Val Asp Phe  
 385 390 395 400  
 Ala Gln Pro Phe Ser Leu Lys Glu Tyr Leu Glu Ser Gln Ser Gln Lys  
 405 410 415  
 Pro Val Ser Ala Leu Leu Ser Leu Glu Gln Ala Leu Leu Pro Ala Ile  
 420 425 430  
 Leu Pro Ser Arg Pro Ser Asp Ala Ala Asp Glu Gly Arg Asp Thr Ser  
 435 440 445  
 Ile Asn Glu Ser Arg Asn Ala Thr Asp Glu Ser Leu Arg Arg Arg Leu  
 450 455 460

Ile	Ala	Asn	Leu	Ala	Glu	His	Ile	Leu	Phe	Thr	Ala	Ser	Lys	Ser	Cys
465					470				475						480
Ala	Ile	Met	Ser	Thr	His	Ile	Val	Ala	Cys	Leu	Leu	Leu	Tyr	Arg	His
				485					490						495
Arg	Gln	Gly	Ile	Asp	Leu	Ser	Thr	Leu	Val	Glu	Asp	Phe	Phe	Val	Met
			500					505					510		
Lys	Glu	Glu	Val	Leu	Ala	Arg	Asp	Phe	Asp	Leu	Gly	Phe	Ser	Gly	Asn
		515					520					525			
Ser	Glu	Asp	Val	Val	Met	His	Ala	Ile	Gln	Leu	Leu	Gly	Asn	Cys	Val
	530					535					540				
Thr	Ile	Thr	His	Thr	Ser	Arg	Asn	Asp	Glu	Phe	Phe	Ile	Thr	Pro	Ser
545					550					555					560
Thr	Thr	Val	Pro	Ser	Val	Phe	Glu	Leu	Asn	Phe	Tyr	Ser	Asn	Gly	Val
				565					570						575
Leu	His	Val	Phe	Ile	Met	Glu	Ala	Ile	Ile	Ala	Cys	Ser	Leu	Tyr	Ala
			580					585						590	
Val	Leu	Asn	Lys	Arg	Gly	Leu	Gly	Gly	Pro	Thr	Ser	Thr	Pro	Pro	Asn
		595					600					605			
Leu	Ile	Ser	Gln	Glu	Gln	Leu	Val	Arg	Lys	Ala	Ala	Ser	Leu	Cys	Tyr
	610					615					620				
Leu	Leu	Ser	Asn	Glu	Gly	Thr	Ile	Ser	Leu	Pro	Cys	Gln	Thr	Phe	Tyr
625					630					635					640
Gln	Val	Cys	His	Glu	Thr	Val	Gly	Lys	Phe	Ile	Gln	Tyr	Gly	Ile	Leu
				645					650						655
Thr	Val	Ala	Glu	His	Asp	Asp	Gln	Glu	Asp	Ile	Ser	Pro	Ser	Leu	Ala
			660					665						670	
Glu	Gln	Gln	Trp	Asp	Lys	Lys	Leu	Pro	Glu	Pro	Leu	Ser	Trp	Arg	Ser
		675					680					685			
Asp	Glu	Glu	Asp	Glu	Asp	Ser	Asp	Phe	Gly	Glu	Glu	Gln	Arg	Asp	Cys
	690					695					700				
Tyr	Leu	Lys	Val	Ser	Gln	Ser	Lys	Glu	His	Gln	Gln	Phe	Ile	Thr	Phe
705					710					715					720
Leu	Gln	Arg	Leu	Leu	Gly	Pro	Leu	Leu	Glu	Ala	Tyr	Ser	Ser	Ala	Ala
			725						730						735
Ile	Phe	Val	His	Asn	Phe	Ser	Gly	Pro	Val	Pro	Glu	Pro	Glu	Tyr	Leu
			740					745					750		
Gln	Lys	Leu	His	Lys	Tyr	Leu	Ile	Thr	Arg	Thr	Glu	Arg	Asn	Val	Ala
		755					760					765			
Val	Tyr	Ala	Glu	Ser	Ala	Thr	Tyr	Cys	Leu	Val	Lys	Asn	Ala	Val	Lys
	770					775					780				
Met	Phe	Lys	Asp	Ile	Gly	Val	Phe	Lys	Glu	Thr	Lys	Gln	Lys	Arg	Val
785					790					795					800
Ser	Val	Leu	Glu	Leu	Ser	Ser	Thr	Phe	Leu	Pro	Gln	Cys	Asn	Arg	Gln
				805					810					815	
Lys	Leu	Leu	Glu	Tyr	Ile	Leu	Ser	Phe	Val	Val	Leu				
			820					825							

<210> 3  
 <211> 2484  
 <212> DNA  
 <213> Homo sapiens

<400> 3  
 atggatgaat ctgcactgac ccttggtaca atagatgttt cttatctgcc acattcatca 60  
 gaatacagtg ttggtcgatg taagcacaca agtgaggaat ggggtgagtg tggctttaga 120  
 cccaccgtct tcagatctgc aactttaaaa tggaaagaaa gcctaataag tgggaaaagg 180  
 ccatttggtg gaagatgttg ttactcctgc actccccaga gctgggacaa atttttcaac 240  
 cccagtatcc cgtctttggg tttgcggaat gttatttata tcaatgaaac tcacacaaga 300  
 caccgaggat ggcttgcaag acgcctttct tacgttcttt ttattcaaga gcgagatgtg 360  
 cataagggca tgtttgccac caatgtgact gaaaatgtgc tgaacagcag tagagtacaa 420  
 gaggaattg cagaagtggc tgctgaatta aaccctgatg gttctgcca gcagcaatca 480  
 aaagccgtta acaaagtga aaagaaagct aaaaggattc ttcaagaaat ggttgccact 540  
 gtctcaccgg caatgatcag actgactggg tgggtgctgc taaaactgtt caacagcttc 600

```

ttttggaaca ttcaaattca caaagggtcaa cttgagatgg ttaaagctgc aactgagacg 660
aatttgccgc ttctgtttct accagttcat agatcccata ttgactatct gctgctcact 720
ttcattctct tctgccataa catcaaagca ccatacattg cttcaggcaa taatctcaac 780
atcccaatct tcagtacctt gatccataag cttgggggct tcttcatacg acgaaggctc 840
gatgaaacac cagatggacg gaaagatgtt ctctatagag ctttgctcca tgggcatata 900
gttgaattac ttcgacagca gcaattcttg gagatcttcc tgggaaggcac acgttctagg 960
agtggaaaaa cctcttgtgc tcgggcagga cttttgtcag ttgtggtaga tactctgtct 1020
accaatgtca tcccagacat cttgataata cctgttggaa tctcctatga tcgcattatc 1080
gaaggtcact acaatggtga acaactgggc aaacctaaaga agaatgagag cctgtggagt 1140
gtagcaagag gtgttattag aatgttacga aaaaactatg gttgtgtccg agtggatttt 1200
gcacagccat tttccttaaa ggaatattta gaaagccaaa gtcagaaacc ggtgtctgct 1260
ctactttccc tggagcaagc gttgttacca gctatacttc cttcaagacc cagtgatgct 1320
gctgatgaag gtagagacac gtccattaat gagtccagaa atgcaacaga tgaatcccta 1380
cgaaggaggt tgattgcaaa tctggctgag catattctat tcaactgctag caagtccctg 1440
gccattatgt ccacacacat tgtggcttgc ctgctcctct acagacacag gcagggaatt 1500
gatctctcca catttggtcga agacttcttt gtgatgaaag aggaagtcct ggctcgtgat 1560
tttgacctgg ggttctcagg aaattcagaa gatgtagtaa tgcattgcat acagctgctg 1620
ggaaattgtg tcacaatcac ccacactagc aggaacgatg agttttttat cacccccagc 1680
acaactgtcc catcagtctt cgaactcaac ttctacagca atgggggtact tcatgtcttt 1740
atcatggagg ccacatagc ttgcagcctt tatgcagttc tgaacaagag gggactgggg 1800
ggtcccacta gcaccccacc taacctgagc agccaggagc agctggtgcg gaaggcgcc 1860
agcctgtgct accttctctc caatgaaggc accatctcac tgccttgcca gacattttac 1920
caagtctgcc atgaaacagt aggaaagttt atccagtatg gcattcttac agtggcagag 1980
cacgatgacc aggaagatat cagtccatgt cttgctgagc agcagtggga caagaagctt 2040
ccagaacctt tgtcttggag aagtgatgaa gaagatgaag acagtgactt tggggaggaa 2100
cagcgagatt gctacctgaa ggtgagccaa tccaaggagc accagcagtt tatcaccttc 2160
ttacagagac tcttggggcc tttgctggag gcctacagct ctgctgccat ctttgttcac 2220
aacttcagtg gtcctgttcc agaacctgag tatctgcaaa agttgcacaa atacctaata 2280
accagaacag aaagaaatgt tgcagtatat gctgagagtg ccacatattg tcttgtgaag 2340
aatgctgtga aaatgtttta ggatattggg gttttcaagg agaccaaaca aaagagagtg 2400
tctgttttag aactgagcag cacttttcta cctcaatgca accgacaaaa acttctagaa 2460
tatattctga gttttgtggt gctg 2484

```

<210> 4  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HMM database acyltransferase domain

<400> 4  
 Asn His Ser Asp Pro Gly Arg Phe Pro Glu Gly Thr Arg Lys Gly Ala  
 1 5 10 15  
 Pro Leu

<210> 5  
 <211> 179  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Prodom database acyltransferase protein

<400> 5  
 Phe Ile Gln Tyr Gly Ile Leu Thr Val Ala Glu Gln Asp Asp Gln Glu  
 1 5 10 15  
 Asp Val Ser Pro Gly Leu Ala Glu Gln Gln Trp Asn Lys Lys Leu Pro  
 20 25 30  
 Glu Pro Leu Asn Trp Arg Ser Asp Glu Glu Asp Glu Asp Ser Asp Phe  
 35 40 45  
 Gly Glu Glu Gln Arg Asp Cys Tyr Leu Lys Val Ser Gln Ala Lys Glu

```

      50      55      60
His Gln Gln Phe Ile Thr Phe Leu Gln Arg Leu Leu Gly Pro Leu Leu
65      70      75      80
Glu Ala Tyr Ser Ser Ala Ala Ile Phe Val His Asn Phe Arg Gly Pro
      85      90      95
Val Pro Glu Ser Glu Tyr Leu Gln Lys Leu His Arg Tyr Leu Ile Thr
      100      105      110
Arg Thr Glu Arg Asn Val Ala Val Tyr Ala Glu Ser Ala Thr Tyr Cys
      115      120      125
Leu Val Lys Asn Ala Val Lys Met Phe Lys Asp Ile Gly Val Phe Lys
      130      135      140
Glu Thr Lys Gln Lys Arg Ala Ser Val Leu Glu Leu Ser Thr Thr Phe
145      150      155      160
Leu Pro Gln Cys Asn Arg Gln Lys Leu Leu Glu Tyr Ile Leu Ser Phe
      165      170      175
Val Val Leu

```

<210> 6  
 <211> 97  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Prodom database acyltransferase protein

```

<400> 6
Met Ser Arg Lys Arg Pro Phe Val Gly Arg Cys Cys Tyr Ser Cys Thr
 1      5      10      15
Pro Gln Ser Trp Glu Arg Phe Phe Asn Pro Ser Ile Pro Ser Leu Gly
      20      25      30
Leu Arg Asn Val Ile Tyr Ile Asn Glu Thr His Thr Arg His Arg Gly
      35      40      45
Trp Leu Ala Arg Arg Leu Ser Tyr Ile Leu Phe Val Gln Glu Arg Asp
      50      55      60
Val His Lys Gly Met Phe Ala Thr Ser Ile Thr Asp Asn Val Leu Asn
65      70      75      80
Ser Ser Arg Val Gln Glu Ala Ile Ala Glu Val Ala Ala Glu Leu Asn
      85      90      95
Pro

```

<210> 7  
 <211> 192  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Prodom database acyltransferase protein

```

<400> 7
Arg Asn Leu Ile Arg Ser Ile Gly Glu His Val Val Phe Asp Cys Ser
 1      5      10      15
Met Met Cys Ser Ile Met Ser Thr His Val Val Ala Cys Leu Leu Leu
      20      25      30
Thr Arg Trp Arg Asn Gly Val His Arg Ser Thr Leu Glu Glu Asp Cys
      35      40      45
Asp Trp Leu Cys Glu Lys Ile Leu Ala Glu Gly Gly Asp Ile Val Gly
      50      55      60
Phe Ser Gly Lys Ser Thr Lys Gly Ser Gln Ile Val Lys Tyr Ala Cys
65      70      75      80
Glu Leu Leu Gly Ser Cys Val Thr Val Thr Asp Glu Asp Arg Asn Asp

```

				85					90					95			
Glu	Phe	Tyr	Ile	Ser	Pro	Lys	Asn	Ser	Val	Pro	Ser	Phe	Ile	Glu	Leu		
			100					105					110				
Ala	Tyr	Tyr	Ser	Asn	Ser	Val	Ile	Cys	His	Phe	Ala	Leu	Lys	Ser	Ile		
		115					120					125					
Ile	Ala	Cys	Thr	Ile	Tyr	Ser	Leu	Pro	Asn	Lys	Thr	Lys	Asn	Gly	Gly		
	130					135					140						
Glu	Ala	Gly	Gly	Leu	Gly	Asn	Leu	Ile	Ser	Gln	Glu	Gln	Leu	Val	Glu		
145				150					155					160			
Asp	Ala	Leu	Ser	Leu	Cys	Asp	Trp	Leu	Gln	Tyr	Glu	Phe	Met	Phe	Cys		
			165					170					175				
Arg	Pro	Cys	Gln	Thr	Leu	Arg	Glu	Leu	Cys	His	Asn	Thr	Leu	Gly	Lys		
			180				185						190				

<210> 8  
 <211> 152  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Prodom database acyltransferase protein

Leu	Ser	Met	Pro	Ile	Met	Gly	Ser	Leu	Leu	Arg	Arg	Thr	Gly	Ala	Phe		
1				5				10					15				
Phe	Ile	Arg	Arg	Ser	Phe	Asp	Pro	Thr	Pro	Glu	Gly	Lys	Gly	Asp	Gln		
		20					25					30					
Leu	Tyr	Arg	Ala	Val	Phe	His	Glu	Tyr	Val	Ala	Gln	Leu	Ile	Ser	Lys		
	35					40					45						
Gly	Tyr	Asn	Ile	Glu	Phe	Phe	Ile	Glu	Gly	Thr	Arg	Ser	Arg	Thr	Gly		
	50				55					60							
Lys	Met	Leu	Pro	Pro	Lys	Thr	Gly	Leu	Leu	Ser	Met	Val	Val	Glu	Ala		
65				70				75						80			
Phe	Leu	Arg	Gly	Ser	Val	Pro	Asp	Ile	Leu	Leu	Val	Pro	Val	Ser	Ile		
			85				90						95				
Ser	Tyr	Asp	Arg	Ile	Ile	Glu	Gly	Asn	Thr	Tyr	Ala	His	Glu	Leu	Arg		
		100					105					110					
Gly	Ala	Pro	Lys	Lys	Glu	Ser	Leu	Trp	Gln	Leu	Phe	Arg	Gly	Val			
	115				120						125						
Arg	Lys	Met	Leu	Lys	Arg	Asn	Tyr	Gly	Gln	Val	Tyr	Val	Asp	Phe	Gly		
	130				135						140						
Glu	Pro	Ile	Ser	Leu	Arg	Glu	Tyr										
145				150													

<210> 9  
 <211> 139  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Prodom database acyltransferase protein

Arg	Asn	Thr	Tyr	Asn	Cys	Ala	Pro	Lys	Arg	Leu	Ala	Leu	Gln	Lys	Met		
1				5				10					15				
Ser	Phe	Glu	Val	Ala	Trp	Arg	Ile	Leu	Gln	Ala	Thr	Pro	Val	Thr	Ala		
		20					25					30					
Thr	Gly	Leu	Val	Ser	Ala	Leu	Leu	Leu	Thr	Thr	Arg	Gly	Thr	Ala	Leu		
	35					40					45						
Thr	Leu	Asp	Gln	Leu	His	His	Thr	Leu	Gln	Asp	Ser	Leu	Asp	Tyr	Leu		
	50				55					60							
Glu	Arg	Lys	Gln	Ser	Pro	Val	Ser	Thr	Ser	Ala	Leu	Arg	Leu	Arg	Ser		

65		70		75		80									
Arg	Glu	Gly	Val	Arg	Ala	Ala	Ala	Asp	Ala	Leu	Ser	Asn	Gly	His	Pro
				85				90						95	
Val	Thr	Arg	Val	Asp	Ser	Gly	Arg	Glu	Pro	Val	Trp	Tyr	Ile	Ala	Pro
			100					105					110		
Asp	Asp	Glu	His	Ala	Ala	Ala	Phe	Tyr	Arg	Asn	Ser	Val	Ile	His	Ala
		115					120					125			
Phe	Leu	Glu	Thr	Ser	Ile	Val	Glu	Leu	Ala	Leu					
	130					135									

<210> 10  
 <211> 123  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Prodom database acyltransferase protein

<400> 10
Asn Leu Lys Lys Asn Val Leu Asn Ser Glu Glu Ile His Tyr Val Ile
1 5 10 15
Glu Gln Glu Ala Lys Glu Ser Ser Thr Ser Ile Asp Lys Val Arg Arg
20 25 30
Glu Ala Arg Glu Ile Leu Asp Glu Met Ser His Thr Leu Asn Met Gly
35 40 45
Met Ile Arg Phe Cys Gly Trp Val Leu Ser Lys Ile Phe Asn Arg Ile
50 55 60
Phe Ser Gly Ile Cys Val Asn Glu Glu Gln Ile Glu Lys Ile Lys Arg
65 70 75 80
Ala Thr Glu Gln Gly His Pro Val Ile Tyr Leu Pro Ser His Arg Ser
85 90 95
His Ile Asp Tyr Leu Leu Leu Ser Phe Ile Leu Tyr His Tyr Asp Ile
100 105 110
Lys Val Pro His Ile Ala Ala Gly Met Asn Leu
115 120

<210> 11  
 <211> 55  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Prodom database acyltransferase protein

<400> 11
Met Glu Glu Ser Ser Val Thr Ile Gly Thr Ile Asp Val Ser Tyr Leu
1 5 10 15
Pro Asn Ser Ser Glu Tyr Ser Leu Gly Arg Cys Lys His Thr Asn Glu
20 25 30
Asp Trp Val Asp Cys Gly Phe Lys Pro Thr Phe Phe Arg Ser Ala Thr
35 40 45
Leu Lys Trp Lys Glu Ser Leu
50 55

<210> 12  
 <211> 123  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Prodom database acyltransferase protein

<400> 12  
Val Asn His Leu Ala Lys Gln Ile Met Thr His Ile Asn Asp Ala Ala  
1 5 10 15  
Ala Val Asn Pro Met Asn Leu Cys Ala Thr Ala Leu Leu Ser Thr Arg  
20 25 30  
Gln Arg Ala Leu Gly Glu Glu Gln Leu Ile Glu Gln Leu Asp Cys Tyr  
35 40 45  
Leu Lys Leu Leu Arg Asn Val Pro Tyr Ser Thr Asp Ala Thr Leu Pro  
50 55 60  
Asp His Thr Pro Glu Arg Leu Ile Glu His Ala Glu Gln Met Asn Leu  
65 70 75 80  
Leu Gly Val Thr Val Glu Lys Asp Thr Leu Gly Asp Ile Leu Arg Leu  
85 90 95  
Asp Arg Asp Asn Ala Val Leu Met Thr Tyr Tyr Arg Asn Asn Val Leu  
100 105 110  
His Leu Phe Ala Leu Pro Ala Leu Val Ala Cys  
115 120

<210> 13  
<211> 91  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Prodom database acyltransferase protein

<400> 13  
Met Thr Tyr Tyr Arg Asn Asn Val Leu His Leu Phe Ala Leu Pro Ala  
1 5 10 15  
Leu Val Ala Cys Phe Lys Asn Asn Arg Arg Ile Ser Arg Asp Ala  
20 25 30  
Leu Leu Arg Phe Val Arg Ala Leu Tyr Pro Phe Leu Gln Ala Glu Leu  
35 40 45  
Phe Leu Arg Trp Asn Glu Asp Glu Leu Asn Asp His Ile Asp Gln Trp  
50 55 60  
Ile Asn Glu Phe Val Arg Gln Gly Leu Leu Leu Ser Ala Gly Asn Gln  
65 70 75 80  
Glu Asp Asp Thr Leu Thr Arg Asn Thr Ser Gln  
85 90

<210> 14  
<211> 110  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Prodom database acyltransferase protein

<400> 14  
Trp Asn Glu Ser Glu Val Leu Val Asp Arg Lys Ser Lys Phe Gln Ala  
1 5 10 15  
Arg Cys Cys Pro Leu Gln Asn Gln Lys Asp Ile Pro Ser Ile Leu Gln  
20 25 30  
Glu Leu Thr Gln Asn Asn Lys Ser Val Ser Lys Ala Ser His Met His  
35 40 45  
Met Tyr Ala Trp Arg Thr Ala Glu Val Ser Asn Asn Leu His Leu Gln  
50 55 60  
Gln Glu Gln Lys Lys Lys Gly Asn Lys Ala Asn Lys Ser Asn Asn Ser  
65 70 75 80  
His Val Asn Lys Ser Arg Asn Ile Thr Val Gln Pro Lys Asn Ile Glu  
85 90 95

Gln Gly Cys Ala Asp Cys Gly Glu Ala Gly Ala Gly Gln Arg  
 100 105 110

<210> 15  
 <211> 827  
 <212> PRT  
 <213> Mus musculus

<220>  
 <223> Prodom database acyltransferase protein

<400> 15  
 Met Glu Glu Ser Ser Val Thr Val Gly Thr Ile Asp Val Ser Tyr Leu  
 1 5 10 15  
 Pro Ser Ser Ser Glu Tyr Ser Leu Gly Arg Cys Lys His Thr Ser Glu  
 20 25 30  
 Asp Trp Val Asp Cys Gly Phe Lys Pro Thr Phe Phe Arg Ser Ala Thr  
 35 40 45  
 Leu Lys Trp Lys Glu Ser Leu Met Ser Arg Lys Arg Pro Phe Val Gly  
 50 55 60  
 Arg Cys Cys Tyr Ser Cys Thr Pro Gln Ser Trp Glu Arg Phe Phe Asn  
 65 70 75 80  
 Pro Ser Ile Pro Ser Leu Gly Leu Arg Asn Val Ile Tyr Ile Asn Glu  
 85 90 95  
 Thr His Thr Arg His Arg Gly Trp Leu Ala Arg Arg Leu Ser Tyr Ile  
 100 105 110  
 Leu Phe Val Gln Glu Arg Asp Val His Lys Gly Met Phe Ala Thr Ser  
 115 120 125  
 Val Thr Glu Asn Val Leu Ser Ser Ser Arg Val Gln Glu Ala Ile Ala  
 130 135 140  
 Glu Val Ala Ala Glu Leu Asn Pro Asp Gly Ser Ala Gln Gln Gln Ser  
 145 150 155 160  
 Lys Ala Ile Gln Lys Val Lys Arg Lys Ala Arg Lys Ile Leu Gln Glu  
 165 170 175  
 Met Val Ala Thr Val Ser Pro Gly Met Ile Arg Leu Thr Gly Trp Val  
 180 185 190  
 Leu Leu Lys Leu Phe Asn Ser Phe Trp Asn Ile Gln Ile His Lys  
 195 200 205  
 Gly Gln Leu Glu Met Val Lys Ala Ala Thr Glu Thr Asn Leu Pro Leu  
 210 215 220  
 Leu Phe Leu Pro Val His Arg Ser His Ile Asp Tyr Leu Leu Leu Thr  
 225 230 235 240  
 Phe Ile Leu Phe Cys His Asn Ile Lys Ala Pro Tyr Ile Ala Ser Gly  
 245 250 255  
 Asn Asn Leu Asn Ile Pro Val Phe Ser Thr Leu Ile His Lys Leu Gly  
 260 265 270  
 Gly Phe Phe Ile Arg Arg Arg Leu Asp Glu Thr Pro Asp Gly Arg Lys  
 275 280 285  
 Asp Ile Leu Tyr Arg Ala Leu Leu His Gly His Val Val Glu Leu Leu  
 290 295 300  
 Arg Gln Gln Gln Phe Leu Glu Ile Phe Leu Glu Gly Thr Arg Ser Arg  
 305 310 315 320  
 Ser Gly Lys Thr Ser Cys Ala Arg Ala Gly Val Leu Ser Val Val Val  
 325 330 335  
 Asn Thr Leu Ser Ser Asn Thr Ile Pro Asp Ile Leu Val Ile Pro Val  
 340 345 350  
 Gly Ile Ser Tyr Asp Arg Ile Ile Glu Gly His Tyr Asn Gly Glu Gln  
 355 360 365  
 Leu Gly Lys Pro Lys Lys Asn Glu Ser Leu Trp Ser Val Ala Arg Gly  
 370 375 380  
 Val Ile Arg Met Leu Arg Lys Asn Tyr Gly Tyr Val Arg Val Asp Phe  
 385 390 395 400  
 Ala Gln Pro Phe Ser Leu Lys Glu Tyr Leu Glu Gly Gln Ser Gln Lys





			20					25					30		
Asp	Trp	Val	Asp	Cys	Gly	Phe	Lys	Pro	Thr	Phe	Phe	Arg	Ser	Ala	Thr
		35					40					45			
Leu	Lys	Trp	Lys	Glu	Ser	Leu	Met	Ser	Arg	Lys	Arg	Pro	Phe	Val	Gly
	50					55					60				
Arg	Cys	Cys	Tyr	Ser	Cys	Thr	Pro	Gln	Ser	Trp	Glu	Arg	Phe	Phe	Asn
	65				70					75					80
Pro	Ser	Ile	Pro	Ser	Leu	Gly	Leu	Arg	Asn	Val	Ile	Tyr	Ile	Asn	Glu
				85					90					95	
Thr	His	Thr	Arg	His	Arg	Gly	Trp	Leu	Ala	Arg	Arg	Leu	Ser	Tyr	Ile
			100					105					110		
Leu	Phe	Val	Gln	Glu	Arg	Asp	Val	His	Lys	Gly	Met	Phe	Ala	Thr	Ser
		115					120					125			
Ile	Thr	Asp	Asn	Val	Leu	Asn	Ser	Ser	Arg	Val	Gln	Glu	Ala	Ile	Ala
	130					135					140				
Glu	Val	Ala	Ala	Glu	Leu	Asn	Pro	Asp	Gly	Ser	Ala	Gln	Gln	Gln	Ser
	145				150					155					160
Lys	Ala	Ile	Gln	Lys	Val	Lys	Arg	Lys	Ala	Arg	Lys	Ile	Leu	Gln	Glu
				165					170					175	
Met	Val	Ala	Thr	Val	Ser	Pro	Gly	Met	Ile	Arg	Leu	Thr	Gly	Trp	Val
			180					185					190		
Leu	Leu	Lys	Leu	Phe	Asn	Ser	Phe	Phe	Trp	Asn	Ile	Gln	Ile	His	Lys
		195					200					205			
Gly	Gln	Leu	Glu	Met	Val	Lys	Ala	Ala	Thr	Glu	Thr	Asn	Leu	Pro	Leu
	210					215					220				
Leu	Phe	Leu	Pro	Val	His	Arg	Ser	His	Ile	Asp	Tyr	Leu	Leu	Leu	Thr
	225				230					235					240
Phe	Ile	Leu	Phe	Cys	His	Asn	Ile	Lys	Ala	Pro	Tyr	Ile	Ala	Ser	Gly
				245					250					255	
Asn	Asn	Leu	Asn	Ile	Pro	Ile	Phe	Ser	Thr	Leu	Ile	His	Lys	Leu	Gly
			260					265					270		
Gly	Phe	Phe	Ile	Arg	Arg	Arg	Leu	Asp	Glu	Thr	Pro	Asp	Gly	Arg	Lys
		275					280					285			
Asp	Ile	Leu	Tyr	Arg	Ala	Leu	Leu	His	Gly	His	Ile	Val	Glu	Leu	Leu
	290					295					300				
Arg	Gln	Gln	Gln	Phe	Leu	Glu	Ile	Phe	Leu	Glu	Gly	Thr	Arg	Ser	Arg
	305				310					315					320
Ser	Gly	Lys	Thr	Ser	Cys	Ala	Arg	Ala	Gly	Leu	Leu	Ser	Val	Val	Val
				325					330					335	
Asp	Thr	Leu	Ser	Ser	Asn	Thr	Ile	Pro	Asp	Ile	Leu	Val	Ile	Pro	Val
			340					345					350		
Gly	Ile	Ser	Tyr	Asp	Arg	Ile	Ile	Glu	Gly	His	Tyr	Asn	Gly	Glu	Gln
		355					360					365			
Leu	Gly	Lys	Pro	Lys	Lys	Asn	Glu	Ser	Leu	Trp	Ser	Val	Ala	Arg	Gly
	370					375	</								

530	Thr	Ile	Thr	His	Thr	Ser	Arg	Lys	Asp	Glu	Phe	540	Phe	Ile	Thr	Pro	Ser
545	Thr	Thr	Val	Pro	Ser	Val	Phe	Glu	Leu	Asn	Phe	555	Tyr	Ser	Asn	Gly	Val
					565							570					575
Leu	His	Val	Phe	Ile	Met	Glu	Ala	Ile	Ile	Ala	Cys	Ser	Leu	Tyr	Ala		
			580					585					590				
Val	Gln	Asn	Lys	Arg	Gly	Ser	Gly	Gly	Pro	Thr	Ser	Thr	Pro	Pro	Asn		
		595					600					605					
Leu	Ile	Ser	Gln	Glu	Gln	Leu	Val	Arg	Lys	Ala	Ala	Ser	Leu	Cys	Tyr		
	610					615					620						
Leu	Leu	Ser	Asn	Glu	Gly	Thr	Ile	Ser	Leu	Pro	Cys	Gln	Thr	Phe	Tyr		
625					630					635					640		
Gln	Val	Cys	Gln	Glu	Thr	Val	Gly	Lys	Phe	Ile	Gln	Tyr	Gly	Ile	Leu		
			645						650					655			
Thr	Val	Ala	Glu	Gln	Asp	Asp	Gln	Glu	Asp	Val	Ser	Pro	Gly	Leu	Ala		
		660					665						670				
Glu	Gln	Gln	Trp	Asn	Lys	Lys	Leu	Pro	Glu	Pro	Leu	Asn	Trp	Arg	Ser		
	675					680					685						
Asp	Glu	Glu	Asp	Glu	Asp	Ser	Asp	Phe	Gly	Glu	Glu	Gln	Arg	Asp	Cys		
	690					695					700						
Tyr	Leu	Lys	Val	Ser	Gln	Ala	Lys	Glu	His	Gln	Gln	Phe	Ile	Thr	Phe		
705					710					715					720		
Leu	Gln	Arg	Leu	Leu	Gly	Pro	Leu	Leu	Glu	Ala	Tyr	Ser	Ser	Ala	Ala		
			725					730						735			
Ile	Phe	Val	His	Thr	Phe	Arg	Gly	Pro	Val	Pro	Glu	Pro	Glu	Tyr	Leu		
		740						745					750				
Gln	Arg	Leu	His	Lys	Tyr	Leu	Ile	Thr	Arg	Thr	Glu	Arg	Asn	Val	Ala		
	755					760					765						
Val	Tyr	Ala	Glu	Ser	Ala	Thr	Tyr	Cys	Leu	Val	Lys	Asn	Ala	Val	Lys		
	770				775					780							
Met	Phe	Lys	Asp	Ile	Gly	Val	Phe	Lys	Glu	Thr	Lys	Gln	Lys	Arg	Ala		
785					790					795					800		
Ser	Val	Leu	Glu	Leu	Ser	Ser	Thr	Phe	Leu	Pro	Gln	Cys	Asn	Arg	Gln		
			805					810						815			
Lys	Leu	Leu	Glu	Tyr	Ile	Leu	Ser	Phe	Val	Val	Leu						
			820					825									